

REMARKS

Of original claims 1-25, claims 5, 13, 22, 24 and 25 are cancelled. Dependent claim 26 has been added. With this response, claims 1-4, 6-12, 14-21, 23 and 26 are now pending.

Applicant does not believe that any fees are due at this time; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to this document, the Commissioner is authorized to deduct the fees from Howrey Simon Arnold & White Deposit Account No. 01-2508/11951.0005.PCUS00.

I. Restriction requirement

The Examiner required restriction under 35 U.S.C. § 121 to:

Group I: Claims 1-12, 14-21, and 23 directed towards nucleotides encoding starch branching enzymes and methods for their use to transform plants for altered starch production, and the resultant transformed plants;

Group II: Claim 13 directed towards isolated amino acid sequences;

Group III: Claim 22 directed towards isolated starch; or

Group IV: Claims 24-25, directed to a method of using starch to produce foodstuffs.

Further, the Examiner indicated that if Group I was elected, Applicants must also elect either a nucleotide sequence encoding SEQ ID NO: 2 (claim 1); a nucleotide sequence comprising SEQ ID NO: 3 (claims 2 and 8); a nucleotide sequence comprising SEQ ID NO: 4 (claims 3 and 8); a nucleotide sequence comprising SEQ ID NO: 5 (claims 4 and 8); a nucleotide sequence comprising SEQ ID NO: 6 (claim 5), or a nucleotide sequence comprising SEQ ID NO:

7 (claim 6). Similarly, it was indicated that if Group II was elected, SEQ ID NO: 2 or one of the proteins encoded by the nucleotide sequences of claims 2-6 must be elected.

In response to the restriction requirement, Applicant elects, with traverse, to continue prosecution of Group I (claims 1-12, 14-21 and 23). Further, Applicants elect a nucleotide encoding SEQ ID NO: 2. The restricted claims 13, 22, 24 and 25 have been cancelled from this application. Applicant may prosecute the non-elected claims in one or more related patent applications.

Notwithstanding the election of Group I claims, Applicants traverse this election to a specific sequence. Each of the nucleotide sequences 3, 4, 5, 9 and 10 presented in claims 1-4 and 8 are 92-97% identical as a class to SBE II-1 (SEQ ID NO: 1), and as such belong to the same group. This is illustrated in the Table below, showing the percent identity of each of SEQ ID NOS: 3-10 with SEQ ID NO: 1, as performed using a BLAST Sequence Comparison (results are attached). Applicants would like to point out that the analysis of SEQ ID NOS: 9 and 10 represents only the identity at the 3' end of SEQ ID NO: 1.

SEQ ID	% Identity with SEQ ID NO: 1
SEQ ID NO: 3	95%
SEQ ID NO: 4	97%
SEQ ID NO: 5	95%
SEQ ID NO: 6	83%
SEQ ID NO: 8	88%
SEQ ID NO: 9	92%
SEQ ID NO: 10	94%

Support for this degree of identity can also be found on pages 9 and 20-21 of the specification, as well as in Table 1 on page 20 and in Figures 3-7. Accordingly, Applicant believes that SEQ ID NOS: 1-5 and 9-10 are drawn to the same invention and should be examined together, and that searching for sequences that have such a high degree of identity would not be unduly burdensome to the Examiner.

As stated in MPEP § 803.04, paragraphs 2-3, a reasonable number of nucleotides can be claimed in a single application. It has been determined that normally ten sequences constitute this reasonable number for examination purposes. Accordingly, because up to ten sequences can be examined in a single application without restriction, Applicants believe that the examination of the seven sequences discussed herein (SEQ ID NOS: 1-5, 9 and 10) is within this reasonable number.

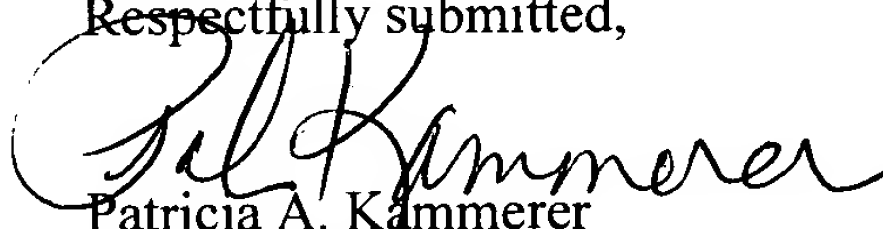
New claim 26 is dependent upon claim 1, and is directed to the nucleotide sequence encoding for the protein in SEQ ID NO. 2.

The Examiner is encouraged to call the undersigned should any further action be required for allowance.

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Date: March 10, 2003

Respectfully submitted,


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Reg. No. 29,775
Attorney for Assignee
MONSANTO UK Ltd.



PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

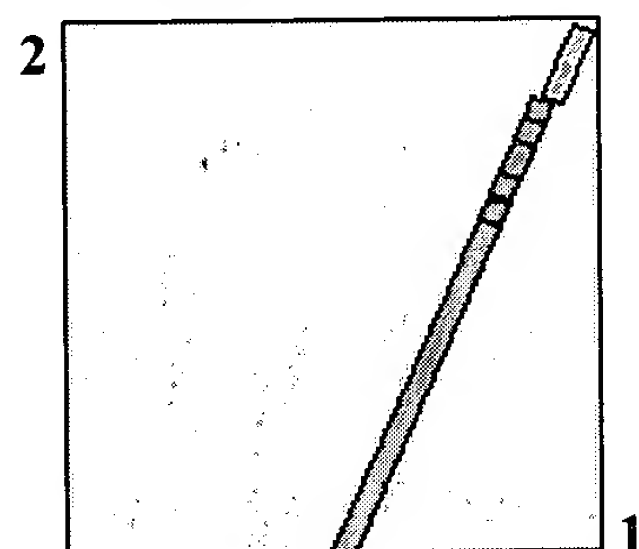
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 1036 (1 .. 1036) 3 (SEQ ID NO: 3)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1396 bits (726), Expect = 0.0
 Identities = 837/879 (95%), Gaps = 12/879 (1%)
 Strand = Plus / Plus



Query: 1184 atgtatgatttcattggctctgaacggaccttcgacacctagtattgatcgtggaatagca 1243
 |||||
 Sbjct: 1 atgtatgatttcattggctctgaacggaccttcgacgcctaattgatcgtggaatagca 60

Query: 1244 ctgcataaaatgattagacttatcacaatgggttttaggaggagagggttatcttaacttt 1303
 |||||
 Sbjct: 61 ctgcataaaatgattanacttatcacaatgggttttaggcggagagggttatcttaacttt 120

Query: 1304 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 1363
 |||||
 Sbjct: 121 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 180

Query: 1364 ccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 1423
 |||||
 Sbjct: 181 ccaagtggtaagttcatcccaggaaacagcaacagttacgacaaatgccgtcgaagattt 240

Query: 1424 gaccagggtgatgcagaatttcttaggtatcatgggtatgcagcagtttgatcaggcgatg 1483
 |||||

.Sbjct: 241 gacctgggtgatgcagaatttcttaggtatcatgggtatgcagcagtttgatcaggcaatg 300

Query: 1484 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtagctatctcgga 1543

|||||

Sbjct: 301 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtagctatctcgga 360

Query: 1544 catgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttgtgttcaacttc 1603

|| |||||

Sbjct: 361 cacgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttgtgttcaacttc 420

Query: 1604 cactggagtaatagctatttctgactaccgggttggtgtttaagcctgggaagtacaag 1663

|||||

Sbjct: 421 cactggagtaatagctatttctgactaccgggtcggtgtttaagcctgggaagtacaag 480

Query: 1664 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 1723

|| |||||

Sbjct: 481 gtggtcttagactcagacgctggactctttggtggatttggtaggatccatcacactgca 540

Query: 1724 gagcacttcacttctgactgccaaacatgacaacaggccccattcggttctcagtgtacact 1783

|||||

Sbjct: 541 gagcacttcacttctgactgccaaacatgacaacaggccccattcggttctcagtgtacact 600

Query: 1784 cctagcagaacctgtgttgtctatgctccaatgaactaaacagcaaagtgcagcatacgc 1843

|||||

Sbjct: 601 cctagcagaacctgtgttgtctatgctccaatgaact-aacagcaaggtgcagcatacgc 659

Query: 1844 atgcacgctgttggtgcttagcactagcaagaaaaaatcgtaggtcaatacaaccagggtg 1903

||| |||||

Sbjct: 660 gtgcgcgctgttggtgcttag---tagcaag-aaaaatcgtaggtcaatacagccagggtg 715

Query: 1904 caaggtttaataagg---gtttgcttcaacgagtcctggatagacaagacaacatgatga 1960

|||||

Sbjct: 716 caaggtttaataaggatttttggcttcaacgagtcctggatagacaagacaacatgatgt 775

Query: 1961 tgtgctctgtgctcccaaattcccagggcggttggtgagaaaaaatgctcatctgtgtt-- 2018

|||||

Sbjct: 776 tgtggcggtgtgctccc-aatccccagggcggttggtgaagaaaacatgctcatctgtgttat 834

Query: 2019 -attttatggatcagggangaaacctccccaaanaccc 2056

|||||

Sbjct: 835 gattttatggatcagcgacgaaacttccccaaataccc 873

Score = 177 bits (92), Expect = 6e-41

Identities = 120/141 (85%)

Strand = Plus / Plus

Query: 2102 atgcctccttaaantttttagccataaaccattgctagtgtcctntaaattgacagttt 2161

```
Query: 2162 agaatagngggtttacttttgtannnnnnnnnnngacagttagactgtattcctcaaataa 2221
      || |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 934 agcatagagggtttacttttgtatcttctttttgacagttagactttattcctcaaataa 993
```

Lambda	K	H
1.33	0.621	1.12

Gapped			
Lambda	K	H	
1.33	0.621	1.12	

```
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 8
Number of Sequences: 0
Number of extensions: 8
Number of successful extensions: 7
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 7,865,278,006
effective HSP length: 26
effective length of query: 2281
effective length of database: 7,865,277,980
effective search space: 17940699072380
effective search space used: 17940699072380
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)
```



PubMed

Entrez

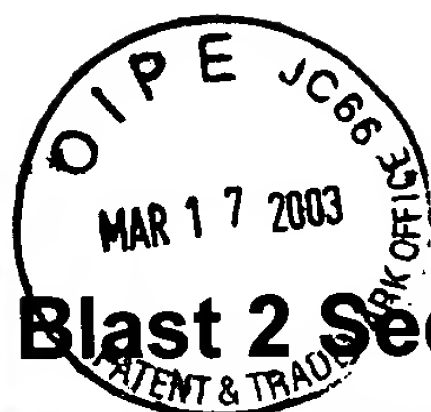
BLAST

OMIM

Taxonomy

Structure

Blast 2 Sequences results

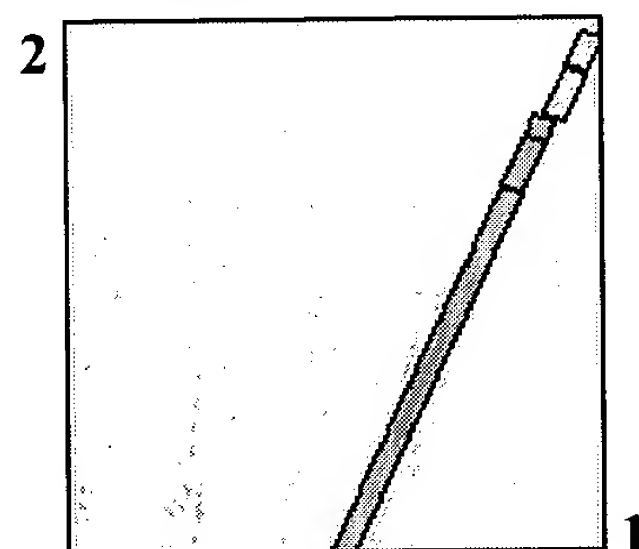


BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 1087 (1 .. 1087) 4 (SEQ ID NO: 4)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1575 bits (819), Expect = 0.0
 Identities = 859/878 (97%), Gaps = 5/878 (0%)
 Strand = Plus / Plus



Query: 1184 atgtatgatttcattggctctgaacggaccttcgacacctagtattgatcgtggaatagca 1243
 |||
 Sbjct: 1 atgtatgatttcattggctctgaacggaccttcgacacctaattgatcgtggaatagca 60

Query: 1244 ctgcataaaatgattagacttatcacaatgggtttaggaggagagggttatcttaacttt 1303
 |||
 Sbjct: 61 ctgcataaaatgattagacttatcacaatgggtttaggaggagagggttatcttaacttt 120

Query: 1304 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 1363
 |||
 Sbjct: 121 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 180

Query: 1364 ccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 1423
 |||
 Sbjct: 181 ccaactggtaagttcatccnngaaacaacaacagttacgacaaatgccgtcgaagattt 240

Query: 1424 gaccagggtgatgcagaatttcttaggtatcatgggtatgcagcagtttgatcaggcgatg 1483
 |||

Sbjct: 241 gacctgggtgatgcagaatttcttaggtatcatgggtatgcagcagtttgatcaggcgatg 300

Query: 1484 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcgaaa 1543
|||||

Sbjct: 301 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcgaaa 360

Query: 1544 catgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttggttcaacttc 1603
|||||

Sbjct: 361 catgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttggttcaacttc 420

Query: 1604 cactggagtaataagctatttcgactaccgggttggtggttaagcctgggaagtacaag 1663
|||||

Sbjct: 421 cactggagtaataagctatttcggtactaccgggttggtggttaagcctgggaagtacaag 480

Query: 1664 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 1723
|||||

Sbjct: 481 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 540

Query: 1724 gagcacttcacttctgactgccaacatgacaacaggccccattcgttctcagtgtacact 1783
|||||

Sbjct: 541 gagcacttcacttctgactgccaacatgacaacaggccccattcgttctcagtgtacact 600

Query: 1784 cctagcagaacctgtgttgctctatgctccaatgaactaaacagcaaagtgcagcatacgc 1843
|||||

Sbjct: 601 cctagcagaacctgtgttgctctatgctccaatgaactaaacagcaaagtgcagcatacgc 660

Query: 1844 atgcacgctggtggtgctagcactagcaagaaaaaatcgatatggtcaatacaaccaggtg 1903
|||||

Sbjct: 661 atgcacgctggtggtgctagcactagcaagaaaaaatcgatatggtcaatacaaccaggtg 720

Query: 1904 caaggtttaataagggt--tttgcttcaacgagtcctggatagacaagacaacatgatgat 1961
|||||

Sbjct: 721 caaggtttaataagggtttttgcttcaacgagtcctggatagacaagacaacatgatgat 780


Query: 1962 gtgctctgtgctcccaaattcccagggcgttggtggagaaaaaatgctcatctgtggt--- 2018
|||||

Sbjct: 781 gtgctctgtgctcccaaattcccagggcgttgngnggaaaacatgctcatctgtgttatc 840

Query: 2019 attttatggatcagggangaaacctcccccaaanaccc 2056
|||||

Sbjct: 841 attttatggatcagngnggaaacctcccccaataaccc 878

Score = 148 bits (77), Expect = 3e-32
Identities = 136/171 (79%), Gaps = 3/171 (1%)
Strand = Plus / Plus



Query: 2102 atgcctccttaaatntttgtagccataaaccattgctagtgtcctntaaattgacagttt 2161

Sbjct: 879 ||||| ||||| | | ||||| |||| | |||| ||||| |||||
atgcctccttaaacttttgtggtcctaaaccatggctactatcctctaaattggcagttt 938

Query: 2162 agaatagnnggttntacttttgtannnnnnnnngacagt---tagactgtattcctcaaa 2218
|| |||| |||| ||||| ||||| ||||| ||||| |||||
Sbjct: 939 agcatagagggttttacttttgtaaatttttttgacagttaatagactctattcctcaaa 998

Query: 2219 taatcgacatggttgtttactcgaagntgagaaataaaatcagagattgnag 2269
|||| ||||| ||||| |||| ||||| ||||| ||||| ||
Sbjct: 999 taattgacatgtcctttacaagaagatgagaaataaaatcagggattgaag 1049

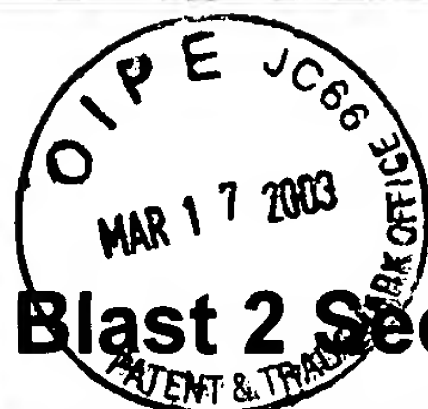
CPU time: 0.10 user secs. 0.04 sys. secs 0.14 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 5
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 7,865,278,006
effective HSP length: 26
effective length of query: 2281
effective length of database: 7,865,277,980
effective search space: 17940699072380
effective search space used: 17940699072380
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

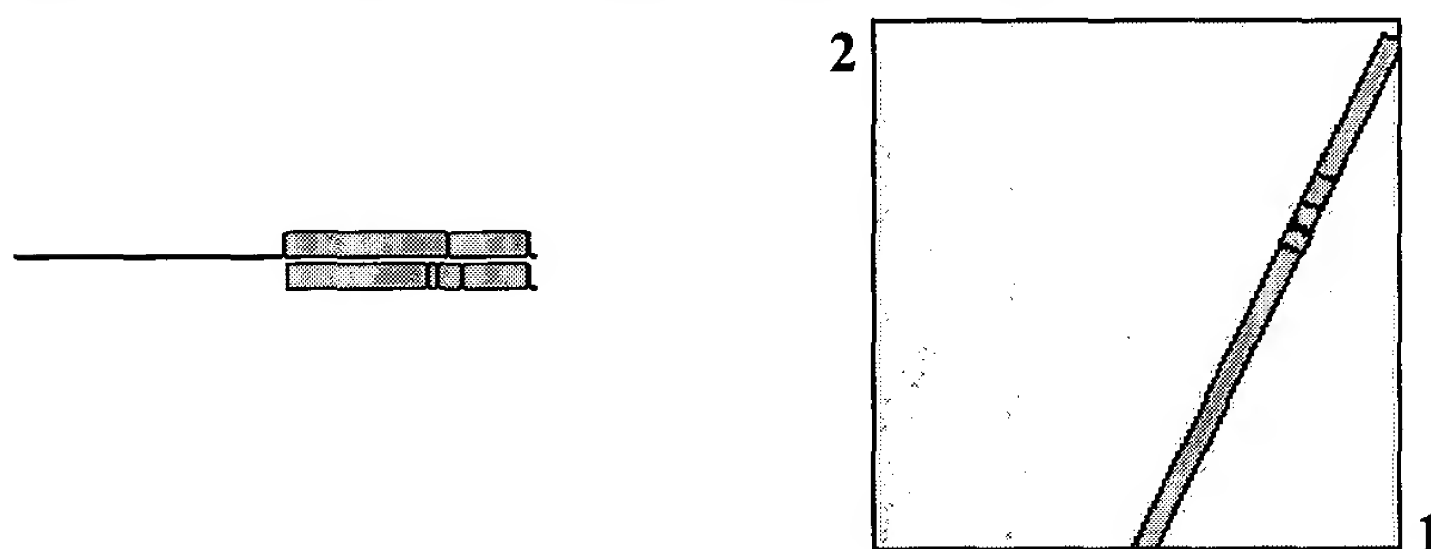
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)
 Sequence 2 lcl|seq_2 Length 1120 (1 .. 1120) 5 (SEQ ID NO: 5)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1742 bits (906), Expect = 0.0
 Identities = 1037/1088 (95%), Gaps = 8/1088 (0%)
 Strand = Plus / Plus

Query: 1184 atgtatgatttcattggtctgaacggaccttcgacacctagtattgatcgtggaatagca 1243
 |||||
 Sbjct: 1 atgtatgatttcattggtctgaacggaccttcgacgcctaattgatcgtggaatagca 60

Query: 1244 ctgcataaaatgattagacttatcacaatgggttaggaggagagggttatcttaacttt 1303
 |||||
 Sbjct: 61 ctgcataaaatgattagacttatcacaatgggtctaggaggagagggttatcttaacttt 120

Query: 1304 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 1363
 |||||
 Sbjct: 121 atgggaaatgagttcgggcatcctgaatggatagactttccaagaggcccacaagtactt 180

Query: 1364 ccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 1423
 |||||
 Sbjct: 181 ccaagtggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagattt 240

Query: 1424 gaccagggtgatgcagaatttcttaggtatcatggtatgcagcagtttgatcaggcgatg 1483
 |||||

Sbjct: 241 gacctgggtgatgcagaatttcttaggtatcatggatgcagcagtttgatcaggcaatg 300

Query: 1484 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcggaaa 1543
|||||
Sbjct: 301 cagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtttctcggaaa 360

Query: 1544 catgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttgtgttcaacttc 1603
|||||
Sbjct: 361 catgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttgtgttcaacttc 420

Query: 1604 cactggagtaataagctatttcgactaccgggttggtgtttaagcctgggaagtacaag 1663
|||||
Sbjct: 421 cactggagtagtagctatttcgactaccgggtcggctgtttaagcctgggaagtacaag 480

Query: 1664 gttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactgca 1723
|| |||||
Sbjct: 481 gtggtcttagactcggacgctggactctttggtggatttggtaggatccatcacactgca 540

Query: 1724 gagcacttcacttctgactgccaaacatgacaacaggcccccattcgttctcagtgtacact 1783
|||||
Sbjct: 541 gagcacttcacttctgactgccaaacatgacaacaggcccccattcattctcagtgtacact 600

Query: 1784 cctagcagaacctgtgttgtctatgctccaatgaactaaacagcaaagtgcagcatacgc 1843
|||||
Sbjct: 601 cctagcagaacctgtgttgtctatgctccaatgaact-aacagcaaagtgcagcatacgc 659

Query: 1844 atgcacgctgttggtgcttagcactagcaagaaaaaatcgtatggtcaatacaaccagggtg 1903
||| |||||
Sbjct: 660 gtgcgcgctgttggtgcttag---tagcaag-aaaaatcgtatggtcaatacaaccagggtg 715

Query: 1904 caaggtttaataagg--gtttgcttcaacgagtcctggatagacaagacaacatgatgat 1961
|||||
Sbjct: 716 caaggtttaataaggatttttgcttcaacgagtcctggatagacaagacaacatgatggt 775

Query: 1962 gtgctctgtgctcccaaattcccagggcggttggtggagaaaaaatgctcatctgtgttatt 2021
|||||
Sbjct: 776 gtgctgtgtgctccc-aatccccagggnggttggaagaaaacatgctcatctgtgttatt 834

Query: 2022 ttatggatcagggangaaacctccccaaanaccccnnnnnnnngaaaggnggatagg 2081
|||||
Sbjct: 835 ttatggatcagggangaaacctccccaaanaccccttttttttttgaaaggnggatagg 894

Query: 2082 cccccggtntctgcatntggatgcctccttaaatntttgtagccataaaccattgctagt 2141
|||||
Sbjct: 895 cccccggtntctgcatntggatgcctccttaaatntttgtagccataaaccattgctagt 954

Query: 2142 gtcctntaaattgacagtttagaatagnngtntacttttgtnnnnnnnnnngacagtt 2201
|||||

.Sbjct: 955 gtcctntaaattgacagtttagaatagnggttntacttttgtattttntttttgacagtt 1014

Query: 2202 agactgtattcctcaaataatcgacatggtgtttactcgaagntgagaaataaaatcaga 2261

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct: 1015 agactgtattcctcaaataatcgacatggtgtttactcgaagntgagaaataaaatcaga 1074

Query: 2262 gattgnag 2269

|||||||

Sbjct: 1075 gattgnag 1082

CPU time: 0.10 user secs. 0.03 sys. secs 0.13 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 7

Number of Sequences: 0

Number of extensions: 7

Number of successful extensions: 5

Number of sequences better than 10.0: 1

length of query: 2307

length of database: 7,865,278,006

effective HSP length: 26

effective length of query: 2281

effective length of database: 7,865,277,980

effective search space: 17940699072380

effective search space used: 17940699072380

T: 0

A: 0

X1: 6 (11.5 bits)

X2: 26 (50.0 bits)

S1: 12 (23.8 bits)

S2: 21 (41.1 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

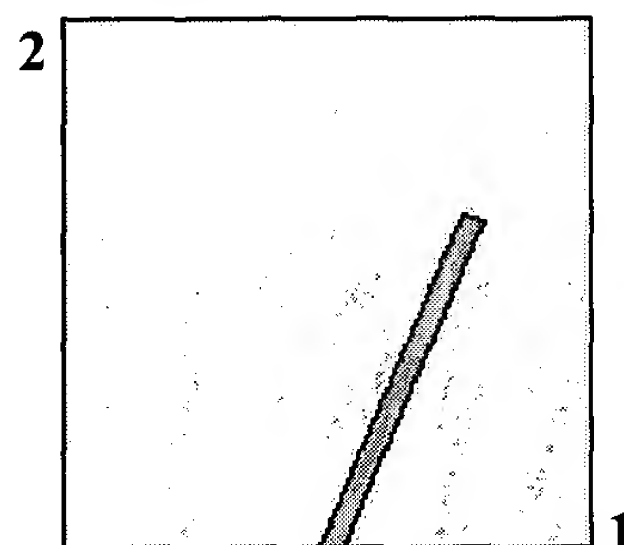
Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)
 Sequence 2 lcl|seq_2 Length 979 (1 .. 979) 6 (SEQ ID NO: 6)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 579 bits (301), Expect = e-162
 Identities = 509/613 (83%)
 Strand = Plus / Plus

Query: 1182 atatgtatgatttcattggctctgaacggaccttcgacacctagtattgatcgtggaatag 1241
 |||||
 Sbjct: 1 atatgtatgatttcattggctctggataggccttcaactcctcgattgatcgtggcatag 60

Query: 1242 cactgcataaaatgattagacttatcacaatgggttttaggaggagagggttatcttaact 1301
 || |
 Sbjct: 61 cattacataaaatgatcaggccttgctaccatgggttttaggtggtgaaggctatcttaact 120

Query: 1302 ttatgggaaatgagttcgggcacacctgaatggatagactttccaagaggcccacaagtac 1361
 |
 Sbjct: 121 tcatgggaaatgagtttgggcacacctgaatggatagattttccaagaggcccacaaactc 180

Query: 1362 ttccaactggtaagttcatcccaggaaacaacaacagttacgacaaatgccgtcgaagat 1421
 |||||
 Sbjct: 181 ttccaaccggcaaagttctccctggaaataacaatagttatgataaatgccgccatagat 240

Query: 1422 ttgaccagggtgatgcagaatttcttaggtatcatggatgcagcagtttgatcaggcga 1481
 |||||

Blast Result

Sbjct: 241 ttgatcttggagatgcagattttcttagatatcgtggtatgcaagagttcgatcaggcaa 300

Query: 1482 tgcagcatcttgaggaaaaatatggctttatgacatcagaccaccagtacgtatctcgga 1541
 |||||

Sbjct: 301 tgcagcatcttgaggaaaaatatgggtttatgacatctgagcaccagtatgtttcacgga 360

Query: 1542 aacatgaggaagataaggtgatcgtgtttgaaaaaggggacttggtatttgtgttcaact 1601
 |||||

Sbjct: 361 aacatgaggaagataaggtgatccttcttcgaaagaggagatttggtatttgttttcaact 420

Query: 1602 tccactggagtaataagctatttcgactaccgggttggtgtttaaagcctgggaagtaca 1661
 |||||

Sbjct: 421 tccactggagcaataagcttttttgactaccgtgttggtgttccaagcctgggaagtaca 480

Query: 1662 aggttgtcttagactcagacgccggactctttggtggatttggtaggatccatcacactg 1721
 |||||

Sbjct: 481 aggtggccttgactccgacgatgcactctttggtggattcagcaggccttgatcatgatg 540

Query: 1722 cagagcacttcacttctgactgccaaacatgacaacaggccccattcgttctcagtgtaca 1781
 |||||

Sbjct: 541 tcgactacttcacaaccgaacatccgcatgacaacaggccgcactctttctcggtgtaca 600

Query: 1782 ctccatgacagaac 1794

|||||

Sbjct: 601 ctccgagcagaac 613

CPU time: 0.09 user secs. 0.03 sys. secs 0.12 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 2
 Number of Sequences: 0
 Number of extensions: 2
 Number of successful extensions: 2
 Number of sequences better than 10.0: 1
 length of query: 2307
 length of database: 7,865,278,006
 effective HSP length: 26
 effective length of query: 2281
 effective length of database: 7,865,277,980
 effective search space: 17940699072380
 effective search space used: 17940699072380
 T: 0
 A: 0
 X1: 6 (11.5 bits)
 X2: 26 (50.0 bits)

Blast Result

S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



PubMed

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Taxonomy

Structure

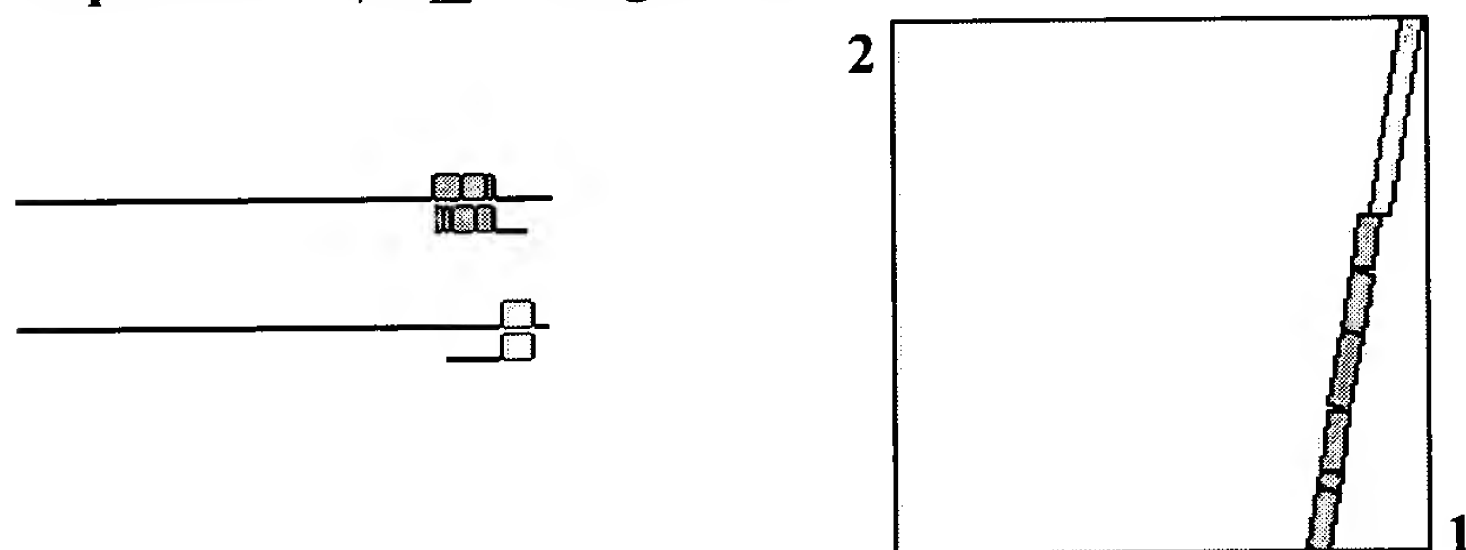
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
x dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 **Length** 378 (1 .. 378) **8** (SEQ ID NO: 8)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 258 bits (134), Expect = 3e-65
Identities = 213/241 (88%), Gaps = 11/241 (4%)
Strand = Plus / Plus



Query: 1822 aacagcaaagtgcagcatatcgcatgcacgctgttgcttagcactagcaagaaaaaatc 1881
||||||| ||||||||| || | ||||||||| |||
Sbjct: 4 aacagcaagggtgcagcatatcgctgcgcgctgttgcttag---tagcaagaaaa-tc 59

Query: 1882 gtatgggtcaataacaaccaggtgcaagggtttaataagggttt---gcttcaacgagtccctg 1938
||| |||||||||| | |||||||||||||||||||| ||| ||||||||||||||||
Sbjct: 60 gtacgggtcaatacagccaggtgcaagggtttaataaggatttttgccttcaacgagtccctg 119

Query: 1939 gatagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcgttgtggag 1998
|||||
Sbjct: 120 gatagacaagacaacatgatg ttgtggcgtgtgctccc-aatccccagggcgttgtgaag 178

```
Query: 1999 aaaaaatgctcatctgtgtt---attttatggatcagggangaaacctccccaaanacc 2055
          ||||| ||||||||||||||||| ||||||||||||||| || ||||| ||||||||| |||
Sbjct: 179  aaacatgctcatctgtgttatgattttatggatcagcgacgaaacttccccaaatacc 238
```

Query: 2056 c 2056

.Sbjct: 239 c 239

Score = 173 bits (90), Expect = 9e-40
Identities = 118/139 (84%)
Strand = Plus / Plus

Query: 2102 atgcctccttaaantntttgtagccataaaccattgctagtgtcctntaaattgacagttt 2161
|||||
Sbjct: 240 atgcctccttaaactttgtggccgtaaaccattgctagtgtcctctaaattgacagttt 299

Query: 2162 agaatagnggttntacttttgtannnnnnnnngacagtttagactgtattcctcaaataa 2221
|| |||
Sbjct: 300 agcatagagggttttacttttgtatcttcttttgacagtttagactttattcctcaaataa 359

Query: 2222 tcgacatggttgtttactcg 2240
||||
Sbjct: 360 tcgaccagtcgtttactcg 378

CPU time: 0.08 user secs. 0.04 sys. secs 0.12 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 7
Number of Sequences: 0
Number of extensions: 7
Number of successful extensions: 6
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 8,015,549,001
effective HSP length: 26
effective length of query: 2281
effective length of database: 8,015,548,975
effective search space: 18283467211975
effective search space used: 18283467211975
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



PubMed

Entrez

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Taxonomy

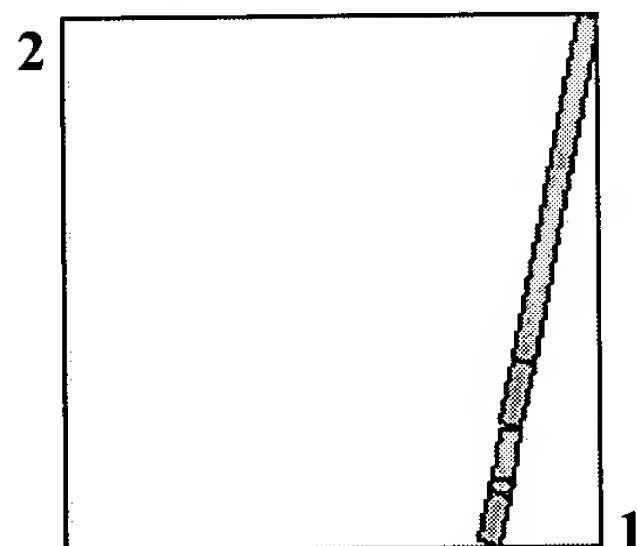
Structure

**Blast 2 Sequences results****BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]**

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lc|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lc|seq_2 Length 449 (1 .. 449) 9 (SEQ ID NO: 9)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 617 bits (321), Expect = e-173
Identities = 415/450 (92%), Gaps = 7/450 (1%)
Strand = Plus / Plus

Query: 1822 aacagcaaagtgcagcatatcgcatgcacgctgttgcttagcactagcaagaaaaaatc 1881
|||||
Sbjct: 5 aacagcaaagtgcagcatatcgctgcgcgctgttgcttag---tagcaagaaaaa-tc 60

Query: 1882 gtatgggtcaatacaaccaggtgcaagggttaataagggttt--gcttcaacgagtcctgg 1939
|||||
Sbjct: 61 gtatgggtcaatacaaccaggtgcaagggttaataaggatttttgcttcaacgagtcctgg 120

Query: 1940 atagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcggttgaggaga 1999
|||||
Sbjct: 121 atagacaagacaacatgatgttgctgtgtgctcccaa-tccccagggngttgtgaaga 179

Query: 2000 aaaaatgctcatctgtgttattttatggatcagggangaaacctccccaaanaccccn 2059
|||
Sbjct: 180 aaacatgctcatctgtgttattttatggatcagggangaaacctccccaaanacccctt 239

Query: 2060 nnnnnnnngaaaggnggataggccccggtnctgcatntggatgcctccttaaatttt 2119
|||||

Sbjct: 240 ttttttttgaaaggnggataggcccccggtntctgcatntggatgcctccttaaantttt 299

Query: 2120 gtagccataaaccattgctagtgctcctntaaattgacagtttagaatagnggttntactt 2179

|||||

Sbjct: 300 gtagccataaaccattgctagtgctcctntaaattgacagtttagaatagnggttntactt 359

Query: 2180 ttgtannnnnnnnngacagtttagactgtattcctcaaataatcgacatggttgtttactc 2239

|||||

Sbjct: 360 ttgtattttntttttgacagtttagactgtattcctcaaataatcgacatggttgtttactc 419

Query: 2240 gaagntgagaaataaaatcagagattgnag 2269

|||||

Sbjct: 420 gaagntgagaaataaaatcagagattgnag 449

CPU time: 0.07 user secs. 0.04 sys. secs 0.11 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 8,015,549,001
effective HSP length: 26
effective length of query: 2281
effective length of database: 8,015,548,975
effective search space: 18283467211975
effective search space used: 18283467211975
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)



Blast 2 Sequences results

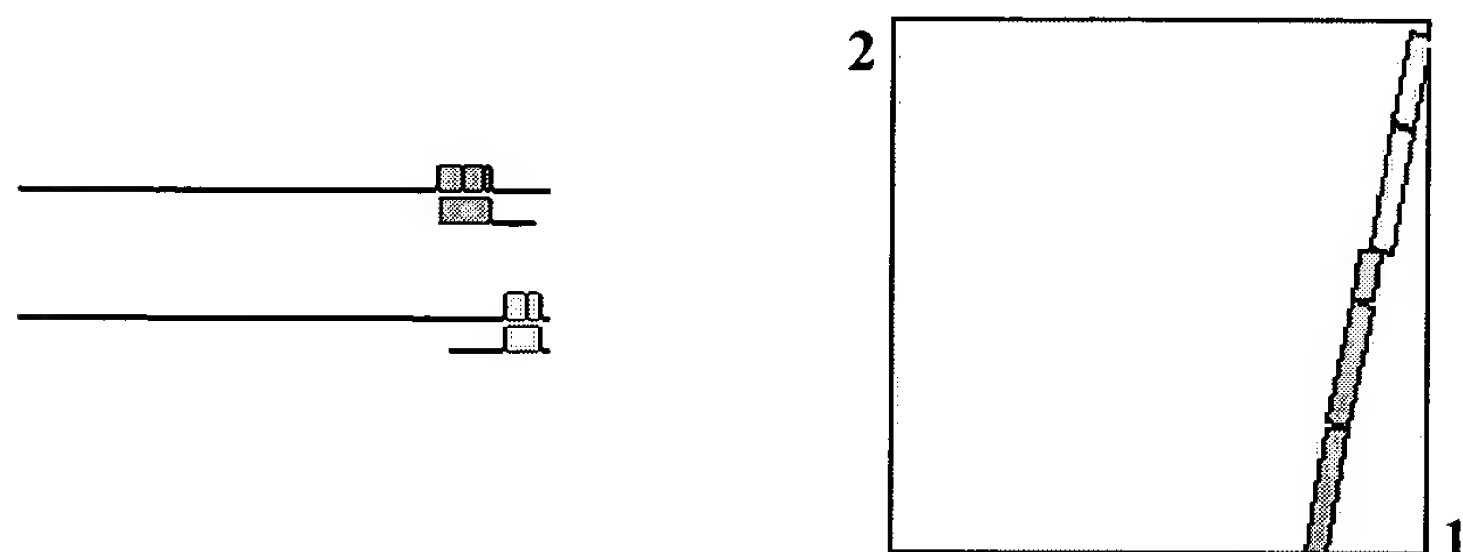
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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lcl|seq_1 Length 2307 (1 .. 2307) 1 (SEQ ID NO: 1)

Sequence 2 lcl|seq_2 Length 428 (1 .. 428) 10 (SEQ ID NO: 10)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 387 bits (201), Expect = e-104
Identities = 231/244 (94%), Gaps = 5/244 (2%)
Strand = Plus / Plus



Query: 1818 actaaacagcaaagtgcagcatatgcacgctgttgcttagcactagcaagaaaa 1877
|||||
Sbjct: 1 actaaacagcaaagtgcagcatatgcacgctgttgcttagcactagcaagaaaa 60

Query: 1878 aatcgtatggtcaatacaaccaggtgcaagggtttaataagg--tttgcttcaacgagtc 1935
|||||
Sbjct: 61 aatcgtatggtcaatacaaccaggtgcaagggtttaataagggtttttgcttcaacgagtc 120

Query: 1936 ctggatagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcggttg 1995
|||||
Sbjct: 121 ctggatagacaagacaacatgatgatgtgctctgtgctcccaaattcccagggcggttg 180

Query: 1996 gagaaaaaatgctcatctgtgtt---attttatggatcagggangaaacctcccccaaan 2052
|||||
Sbjct: 181 nggaaaacatgctcatctgtgttatcattttatggatcagngnggaaacctcccccaaat 240

Query: 2053 accc 2056
||||

Sbjct: 241 accc 244

Score = 148 bits (77), Expect = 3e-32
Identities = 136/171 (79%), Gaps = 3/171 (1%)
Strand = Plus / Plus

Query: 2102 atgcctccttaaatntttgtagccataaaccattgctagtgtcctntaaattgacagttt 2161
||||| ||||| | | ||||| |||| | ||| ||||| |||||
Sbjct: 245 atgcctccttaaaccttttgtggtcctaaaccatggctactatcctctaaattggcagttt 304

Query: 2162 agaatagngggtntactttttgtannnnnnnnngacagt---tagactgtattcctcaaa 2218
|| |||| |||| ||||| ||||| ||||| ||||| |||||
Sbjct: 305 agcatagagggtttactttttgtaaatttttttgacagttaatagactctattcctcaaa 364

Query: 2219 taatcgacatgttggtttactcgaagntgagaaataaaatcagagattgnag 2269
|||| ||||| |||| | ||| ||||| ||||| ||||| ||
Sbjct: 365 taattgacatgtcctttacaagaagatgagaaataaaatcagggattgaag 415

CPU time: 0.09 user secs. 0.03 sys. secs 0.12 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 6
Number of Sequences: 0
Number of extensions: 6
Number of successful extensions: 5
Number of sequences better than 10.0: 1
length of query: 2307
length of database: 8,015,549,001
effective HSP length: 26
effective length of query: 2281
effective length of database: 8,015,548,975
effective search space: 18283467211975
effective search space used: 18283467211975
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)